Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1 - 24 (canceled).

25 (currently amended). A method of targeted sequence alteration of a nucleic acid present within selectively enriched cells **in vitro**, cells in culture, or cell-free extracts, comprising:

combining the targeted nucleic acid in the presence of cellular repair proteins with a single-stranded nonhairpin oligonucleotide 17 - 121 nucleotides in length, said oligonucleotide having a domain of at least 8 contiguous deoxyribonucleotides,

wherein said oligonucleotide is fully complementary in sequence to the sequence of a first strand of the nucleic acid target, but for one or more mismatches as between the sequences of said deoxyribonucleotide domain and its complement on the target nucleic acid first strand, each of said mismatches positioned at least 8 nucleotides from said oligonucleotide's 5' and 3' termini;

wherein said oligonucleotide has at least one terminal modification selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages, and

wherein said cultured or selectively enriched cells are not human embryonic stem cells.

26 (previously presented). The method of claim 25, wherein said sequence alteration is a substitution of at least one base.

27 (previously presented). The method of claim 25, wherein said sequence alteration is a deletion of at least one base.

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28 (previously presented). The method of claim 25, wherein said alteration is an insertion of at least one base.

29 (previously presented). The method of claim 25, wherein said target nucleic acid is DNA.

30 (previously presented). The method of claim 29, wherein said DNA is double-stranded DNA.

31 (previously presented). The method of claim 30, wherein said double-stranded DNA is genomic DNA.

32 (previously presented). The method of claim 31, wherein said genomic DNA is in a chromosome.

33 (previously presented). The method of claim 32, wherein said chromosome is an artificial chromosome.

34 (previously presented). The method of claim 31, wherein said genomic DNA is episomal.

35 (currently amended). The method of claim 25, wherein said cellular **repair** proteins are purified.

36 (currently amended). The method of claim 25, wherein said cellular **repair** proteins are present in a cell-free protein extract.

37 (currently amended). The method of claim 25, wherein said cellular **repair** proteins are present within an intact cell.

38 (previously presented). The method of claim 37, wherein said cell is cultured *ex vivo*.

39 (canceled).

40 (currently amended). The method of claim 25, wherein said **cellular repair** proteins are of a cell selected from the group consisting of: prokaryotic cells and eukaryotic cells.

41 (previously presented). The method of claim 40, wherein said cell is a prokaryotic cell.

42 (previously presented). The method of claim 41, wherein said prokaryotic cell is a bacterial cell.

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43 (previously presented). The method of claim 42, wherein said bacterial cell is an *E. coli* cell.

44 (previously presented). The method of claim 40, wherein said cell is a eukaryotic cell.

45 (previously presented). The method of claim 44, wherein said eukaryotic cell is a yeast cell, plant cell, human cell, or a mammalian cell.

46 (previously presented). The method of claim 45, wherein said eukaryotic cell is a yeast cell.

47 (currently amended). The method of claim 46, wherein said yeast **cell** is **a** *Saccharomyces cerevisiae*, *Ustilago maydis*, or *Candida albicans* **cell**.

48 (previously presented). The method of claim 45, wherein said eukaryotic cell is a plant cell.

49 (previously presented). The method of claim 45, wherein said eukaryotic cell is a human cell.

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50 (previously presented). The method of claim 49, wherein said human cell is selected from the group consisting of liver cell, lung cell, colon cell, cervical cell, kidney cell, epithelial cell, cancer cell, and stem cell.

51 (previously presented). The method of claim 45, wherein said eukaryotic cell is from a mammal.

52 (previously presented). The method of claim 51, wherein said mammal is selected from the group consisting of: rodent, mouse, hamster, rat, and monkey.

53 (previously presented). The method of claim 25, wherein said oligonucleotide is at least 25 nucleotides in length.

54 (previously presented). The method of claim 25, wherein said oligonucleotide is no more than 74 nucleotides in length.

55 (canceled).

56 (previously presented). The method of claim 25, wherein said first strand is the nontranscribed strand of the target nucleic acid.

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57 (currently amended). The method of claim 25, wherein the sequences of said ~~internally unduplexed~~ deoxyribonucleotide domain and of the target nucleic acid first strand are mismatched at a single nucleotide.

58 (currently amended). The method of claim 25, wherein the sequences of said ~~internally unduplexed~~ deoxyribonucleotide domain and of its complement on the target nucleic acid first strand are mismatched at two or more nucleotides.

59 (previously presented). The method of claim 25, wherein said at least one terminal modification is at least one 3' terminal LNA analogue.

60 (previously presented). The method of claim 59, wherein said oligonucleotide has no more than 3 LNA analogues at its 3' terminus.

61 (previously presented). The method of claim 59, wherein said oligonucleotide has at least one LNA at its 3' terminus and at least one LNA at its 5' terminus.

62 (previously presented). The method of claim 61, wherein said oligonucleotide has no more than 3 contiguous LNA at each of its 3' or 5' termini.

63 (previously presented). The method of claim 25, wherein said at least one terminal modification is at least one 2'-O-methyl ribonucleotide analog at its 3' terminus.

64 (previously presented). The method of claim 63, wherein said oligonucleotide has no more than 4 contiguous 2'-O-methyl ribonucleotide analogs.

65 (previously presented). The method of claim 63, wherein said oligonucleotide has at least one 2'-O-methyl ribonucleotide analog at its 3' terminus and at least one 2'-O-methyl ribonucleotide analog at its 5' terminus.

66 (previously presented). The method of claim 65, wherein said oligonucleotide has no more than 4 contiguous 2'-O-methyl ribonucleotide analogs.

67 (previously presented). The method of claim 25, wherein said at least one terminal modification comprises at least three terminal phosphorothioate linkages.

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69 (previously presented). The method of claim 67, wherein said oligonucleotide comprises no more than 6 contiguous phosphorothioate linkages.

70 (previously presented). The method of claim 25, wherein said targeted nucleic acid is selected from the group of human genes consisting of: ADA, p53, beta-globin, RB, BRCA1, BRCA2, CFTR, CDKN2A, APC, Factor V, Factor VIII, Factor IX, hemoglobin alpha 1, hemoglobin alpha 2, MLH1, MSH2, MSH6, ApoE, LDL receptor, UGT1, APP, PSEN1, and PSEN2.

71 (previously presented). The method of claim 70, wherein said targeted nucleic acid is the human beta-globin gene.

72 (previously presented). The method of claim 71, wherein said human beta-globin gene is targeted in a human hematopoietic stem cell.

73 (previously presented). The method of claim 25, wherein said oligonucleotide is 17 - 121 nucleotides in length and includes the sequence of any one of SEQ ID NOs: 1 - 4340.

74 (previously presented). The method of claim 73, wherein said oligonucleotide has sequence identical to any one of SEQ ID NOs: 1 - 4340.

75 (currently amended). A method of targeted sequence alteration of a nucleic acid present within selectively enriched cells **in vitro**, cells in culture, or cell-free extracts, comprising:

combining the targeted nucleic acid in the presence of cellular repair proteins with a single-stranded nonhairpin oligonucleotide 17 - 121 nucleotides in length, said oligonucleotide having a domain of at least 8 contiguous deoxyribonucleotides,

wherein said oligonucleotide is fully complementary in sequence to the sequence of a first strand of the nucleic acid target, but for one or more mismatches as between the sequences of said deoxyribonucleotide domain and its complement on the target nucleic acid first strand, each of said mismatches positioned at least 8 nucleotides from said oligonucleotide's 5' and 3' termini;

wherein said oligonucleotide has at least one terminal modification, said oligonucleotide includes the sequence of any one of SEQ ID NOs: 1 - 4340, and said cultured or selectively enriched cells are not human embryonic stem cells.

76 (previously presented). The method of claim 75, wherein said at least one terminal modification is selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

77 (previously presented). The method of claim 75, wherein said target is chromosomal genomic DNA.

78 (new). A method of targeted sequence alteration of a nucleic acid present within selectively enriched hematopoietic stem cells in vitro or hematopoietic stem cells in culture, comprising:

combining the targeted nucleic acid in the presence of cellular repair proteins with a single-stranded nonhairpin oligonucleotide 17 - 121 nucleotides in length, said oligonucleotide having a domain of at least 8 contiguous deoxyribonucleotides,

wherein said oligonucleotide is fully complementary in sequence to the sequence of a first strand of the nucleic acid target, but for one or more mismatches as between the sequences of said deoxyribonucleotide domain and its complement on the target nucleic acid first strand, each of said mismatches positioned at least 8 nucleotides from said oligonucleotide's 5' and 3' termini; and

wherein said oligonucleotide has at least one terminal modification selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.